

AMENDMENT: IN THE SPECIFICATION

Please enter the Sequence Listing into the application.

1. Please replace the paragraph [0059] with the following amended paragraph:

[0001] Although the GTPases are employed in a variety of diverse functions, they are characterized by highly conserved sequence motifs (i.e., shared structural characteristics that define the genus) that encode the guanine nucleotide-binding domain (see, for example, Bourne et al. (1991) "The GTPase superfamily: conserved structure and molecular mechanism" Nature 349:117-27). For example, Table 1 illustrates a partial alignment of 9 exemplary GTPases showing amino acid subsequences which comprise part of the substrate binding site.

Table 1. Partial amino acid sequence alignment of exemplary GTPases.

GTPase	position	amino acid subsequence	position	amino acid subsequence
H-Ras	10	GAGGVGKSALTI (SEQ ID NO:35)	113	LVGNKCD (SEQ ID NO:36)
Rab7	15	GDSGVGKTSLMN (SEQ ID NO:37)	122	VLGNKID (SEQ ID NO:38)
Ran	17	GDGGTGKTTFVK (SEQ ID NO:39)	119	LCGNKVD (SEQ ID NO:40)
Ra1B	21	GSGGVGKSALT (SEQ ID NO:41)	125	VVGNKSD (SEQ ID NO:42)
Rap1B	10	GSGGVGKSALT (SEQ ID NO:43)	113	LVGNKCD (SEQ ID NO:44)
RhoA	12	GDGACGKTCLLI (SEQ ID NO:45)	114	LVGNKKD (SEQ ID NO:46)
Arf4	27	GLDCAGKTTVLY (SEQ ID NO:47)	131	IVANKQD (SEQ ID NO:48)
G _t	40	GAGESGKSTIVK (SEQ ID NO:49)	266	LFLNKKD (SEQ ID NO:50)
EF1A	14	GHVDSGKSTTTG (SEQ ID NO:51)	150	VGVNKMD (SEQ ID NO:52)